

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Douglas A. Holtzman et al. Art Unit : Unknown
Serial No. : Unassigned Examiner : Unknown
Filed : Herewith
Title : NOVEL GENES ENCODING PROTEINS HAVING PROGNASTIC,
DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER USES

Box Patent Application
Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 CFR §1.821(f)

I hereby state, as required by 37 C.F.R. §1.821(f), that the content of the paper and computer-readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §§1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Date: March 16, 2001

for



Anita L. Meiklejohn, Ph.D.
Reg. No. 35,283

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20164827.doc

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EL298429675US

I hereby certify under 37 CFR §1.10 that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

March 16, 2001
Date of Deposit

USA G. Gray
Signature

USA G. Gray
Typed or Printed Name of Person Signing Certificate

SEQUENCE LISTING

<110> Holtzman, Douglas A.
 Gearing, David P.
 Pan, Yang

<120> NOVEL GENES ENCODING PROTEINS HAVING
 PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER
 USES

<130> 07334-324001

<150> US 09/712,726

<151> 2000-11-14

<150> US 08/820,364

<151> 1997-03-12

<150> US 09/757,421

<151> 2001-01-10

<150> US 08/843,652

<151> 1997-04-16

<150> US 08/843,651

<151> 1997-04-16

<150> US 09/354,809

<151> 1999-07-16

<150> US 08/938,365

<151> 1997-09-26

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 755

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(279)

<400> 1

atg gct cgc cta cag act gca ctc ctg gtt gtc ctc gtc ctc ctt gct	48
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala	
1 5 10 15	

gtg gcg ctt caa gca act gag gca ggc ccc tac ggc gcc aac atg gaa	96
Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu	
20 25 30	

gac agc gtc tgc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg cgc	144
---	-----

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 35 40 45

gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct ggc 192
 Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 50 55 60

gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc aga 240
 Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
 65 70 75 80

gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa tgaagagcct 289
 Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 85 90

actctgatga ccgtggcctt ggctcctcca ggaaggctca ggagccctac ctccctgcca 349
 ttatagctgc tccccgccag aagcctgtgc caactctctg cattccctga tctccatccc 409
 tgtggctgtc acccttgggtc acctccgtgc tgtcactgcc atctcccccc tgaccctct 469
 aaccctaccc ctgcctccct ccttgcagtc agagggtcct gttcccatca gcgattcccc 529
 tgettaaacc cttccatgac tccccactgc cctaagctga ggtcagtcct ccaagcctgg 589
 catgtggccc tctggatctg ggttccattt ctgtctccag cctgcccact tcccttcattg 649
 aatgttgggt tctagctccc tgttctccaa acccatacta cacatccac ttctgggtct 709
 ttgcctggga tgttgcgtgac actcagaaag tcccgtcgac gcggcc 755

<210> 2
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
 1 5 10 15
 Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
 20 25 30
 Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 35 40 45
 Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 50 55 60
 Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
 65 70 75 80
 Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 85 90

<210> 3
 <211> 4051
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128)...(1447)

<221> misc_feature
 <222> (1)...(4051)
 <223> n = A,T,C or G

<400> 3

gtcgacccac gcgtccggcc ggagaacccg caatctttgc gccacaaaa tacaccgacg	60
atgcccgatc tactttaagg gctgaaaccc acgggcctga gagactataa gagcggtccc	120
taccgcc atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc	169
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala	
1 5 10	
cgg aaa agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct	217
Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro	
15 20 25 30	
ggg ctc cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg	265
Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu	
35 40 45	
ctg ttg gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct	313
Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala	
50 55 60	
ccc cag cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag	361
Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu	
65 70 75	
gga ttg tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc	409
Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys	
80 85 90	
atc tcc tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc	457
Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu	
95 100 105 110	
ctt ttc tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta	505
Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu	
115 120 125	
agt ccc tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc	553
Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly	
130 135 140	
acc ttc cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca	601
Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr	
145 150 155	
ggg tgt ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt	649
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser	
160 165 170	
gac atc gaa tgt gtc cac aaa gaa tca ggt ata aag cac agt ggg gaa	697
Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Lys His Ser Gly Glu	
175 180 185 190	
gcc cca gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc	745
Ala Pro Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala	
195 200 205	
tct ccc tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc	793
Ser Pro Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala	
210 215 220	

gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys 225 230 235	841
aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp 240 245 250	889
cct gag cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn 255 260 265 270	937
gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu 275 280 285	985
cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met 290 295 300	1033
ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu 305 310 315	1081
agg tct cag agg agg agg ctg ctg gtt cca gca att gaa ggt gat ccc Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Ile Glu Gly Asp Pro 320 325 330	1129
act gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro 335 340 345 350	1177
ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn 355 360 365	1225
gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu 370 375 380	1273
tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser 385 390 395	1321
gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala 400 405 410	1369
aag cag aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr 415 420 425 430	1417
cta gaa ggt aat gca gac tct gcc atg tcc taagtgtgat tctcttcagg Leu Glu Gly Asn Ala Asp Ser Ala Met Ser 435 440	1467

```

aagtgaagacc ttccctgggt tacctttttt ctggaaaaag cccaactgga ctccagtcag 1527
taggaaagtg ccacaattgt cacatgaccg gtactggaag aaactctccc atccaacatc 1587
acccagtgga tggaacatcc tgtaactttt cactgcactt ggcatatttt ttataagctg 1647
aatgtgataa taaggacact atggaaatgt ctggatcatt ccgtttgtgc gtactttgag 1707
atttggtttg ggatgtcatt gttttcacag cactttttta tcctaattgt aatgctttat 1767
ttattttattt gggctacatt gtaagatcca tctacacagt cgttgtccga cttcacttga 1827
tactatatga tatgaacctt ttttgggtgg ggggtgcngg gcaattccac tctgtctccc 1887
aggctggagt gcaatgggtg aatcttggct cactatagcc ttgacctctg aggctcaagc 1947
gattctctca cctcagccat ccaaatagct gggaccacag gtgtgcacca ccacgcccgg 2007
ctaatttttt gtattttgtc taaatataag ggctctctat gttgtctcagg gtggtctcga 2067
attcctggac tcaagcagtc tgcccacytc agactcccaa agcgggtggaa ttagargcgt 2127
gagcccccat gcttggcctt acctttctac yttttataat tctgtatgtt attattttat 2187
gaacatgaag aaactttagt aaatgtactt gtttacatag ttatgtgaat agattagata 2247
aacataaaaag gaggagacat acaatggggg aagaagaaga agtcccctgt aagaagttna 2307
cgntctgggt tccagccttc cctcagatgt actttggctt caatgattgg caactcttac 2367
agggggccagt cttttgaact ggacaacctt acaagtatat gagtattatt tataggtagt 2427
tgtttacata tgagtcggga ccaaagagaa ctggatccac gtgaagtcct gtgtgtggct 2487
gggtccctacc tgggcagtc catttgcacc catagcccc atctatggac aggctgggac 2547
agaggcagat gggtagatc acacataaca ataggggtcta tgtcatatcc caagtgaact 2607
tgagccctgt ttgggtcag gagatagaag aaaaaatctg tctcccacgt ctgccatggc 2667
atcaaggggg aagagtagat ggtgcttgag aatgggtgtga aatgggtgtg atctcaggag 2727
tagatggccc ggctcacttc tggttatctg tcacctgag cccatgagct gccttttagg 2787
gtacagattg cctacttgag gaccttggc gctctgtaag catctgactc atctcagaaa 2847
tgtcaattct taaacactgt ggcaacagga cctagaatgg ctgacgcatt aaggttttct 2907
tcttgtgtcc tgttctatta ttgttttaag acctcagtaa ccatttcagc ctctttccag 2967
caaacacctt tccatagtat ttcagtcatg gaaggatcat ttatgcagg agtcattcca 3027
ggagtttttg gtcttttctg tctcaaggca ttgtgtgttt tgttccggga ctggtttggg 3087
tgggacaaaag ttagaattgc ctgaagatca cacattcaga ctgttgtgtc tgtggagttt 3147
taggagtggg gggtagcctt tctgggtctt gcacttccat cctctcccac ttccatctgg 3207
catcccacgc gttgtcccct gcacttctgg aaggcacagg gtgctgctgc ctctggtct 3267
ttgcctttgc tgggccttct gtgcaggacg ctcagcctca gggctcagaa ggtgccagtc 3327
cggctccagg tcccttgtcc cttccacaga ggccttcccta gaagatgcat ctagagtgtc 3387
agccttatca gtgtttaaga tttttctttt atttttaatt tttttgagac agaattctac 3447
tctctcgccc aggctggagt gcaacggtag gatcttggct cagtgaacc tccgcctcct 3507
gggttcaagc gattctcgtg cctcagcctc cggagtagct gggattgcag gcaccgcca 3567
ccacgcctgg ttaatttttg tatttttagt agagacgggg tttcaccatg ttggtcaggc 3627
tggctcgaac ctctgacct caggtagatc accttggcct ccgaaagtgc tgggattaca 3687
ggcgtgagcc accagccagg ccaagctatt cttttaaagt aagcttctg acgacatgaa 3747
ataattgggg gttttgttgt ttagttacat taggctttgc tatatccca ggccaaatag 3807
catgtgacac aggacagcca tagtatagtg tgtcactcgt ggttggtgtc ctttcatgct 3867
tctgccctgt caaaggtccc tatttgaaat gtgttataat acaaacagg aagcacattg 3927
tgtacaaaat acttatgtat ttatgaatcc atgaccaa ataatatgaa acctatata 3987
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggsgggcgg 4047
ccgc 4051

```

<210> 4

<211> 440

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
  1           5           10           15
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
      20           25           30
Arg Val Pro Lys Thr Leu Val Leu Val Ala Ala Val Leu Leu Leu
      35           40           45

```

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60
 Gln Arg Ala Ala Pro Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 100 105 110
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175
 Glu Cys Val His Lys Glu Ser Gly Ile Lys His Ser Gly Glu Ala Pro
 180 185 190
 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
 195 200 205
 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
 210 215 220
 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
 225 230 235 240
 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
 245 250 255
 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
 260 265 270
 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
 275 280 285
 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
 290 295 300
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
 305 310 315 320
 Gln Arg Arg Arg Leu Leu Val Pro Ala Ile Glu Gly Asp Pro Thr Glu
 325 330 335
 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
 340 345 350
 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
 355 360 365
 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
 370 375 380
 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
 385 390 395 400
 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
 405 410 415
 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
 420 425 430
 Gly Asn Ala Asp Ser Ala Met Ser
 435 440

<210> 5

<211> 3964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
 <222> (128)...(1360)

<221> misc_feature
 <222> (1)...(3964)
 <223> n = A,T,C or G

```

<400> 5
gtcgacccac gcgtccggcc ggagaacccg caatctttgc gcccacaaaa tacaccgacg      60
atgcccgatc tactttaagg gctgaaaccc acgggcctga gagactataa gagcgttccc      120
taccgcc atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc      169
      Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala
              1              5              10

cgg aaa agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct      217
Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
      15              20              25              30

ggg ctc cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg      265
Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu
              35              40              45

ctg ttg gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct      313
Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala
              50              55              60

ccc cag cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag      361
Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu
              65              70              75

gga ttg tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc      409
Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys
              80              85              90

atc tcc tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc      457
Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu
              95              100              105              110

ctt ttc tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta      505
Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu
              115              120              125

agt ccc tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc      553
Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly
              130              135              140

acc ttc cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca      601
Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
              145              150              155

ggg tgt ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt      649
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser
              160              165              170

gac atc gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca      697
Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr
              175              180              185              190

```


gtt gca gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta	745
Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu	
195 200 205	
ctg tgg aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt	793
Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly	
210 215 220	
ggg ggg gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct	841
Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala	
225 230 235	
gag gac aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag	889
Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln	
240 245 250	
gtc cct gag cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt	937
Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly	
255 260 265 270	
gtc aac atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca	985
Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala	
275 280 285	
gaa gct gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa	1033
Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu	
290 295 300	
ggg gat ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac	1081
Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp	
305 310 315	
ttg gtg ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc	1129
Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu	
320 325 330	
atg gac aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg	1177
Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg	
335 340 345 350	
gac acc ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga	1225
Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg	
355 360 365	
gat gcc tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag	1273
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu	
370 375 380	
aga ctt gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag	1321
Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys	
385 390 395	
ttc atg tat cta gaa ggt aat gca gac tct gcc atg tcc taagtgtgat	1370
Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser	
400 405 410	

```

tctcttcagg aagtgagacc ttccctgggt tacctttttt ctggaaaaag cccaactgga 1430
ctccagtcag taggaaagt ccacaattgt cacatgaccg gtactggaag aaactctccc 1490
atccaacatc acccagtgga tggaacatcc tgtaactttt cactgcactt ggcattattt 1550
ttataagctg aatgtgataa taaggacact atggaaatgt ctggatcatt ccgtttgtgc 1610
gtacttttag atttggtttg ggatgtcatt gttttcacag cactttttta tcctaattgta 1670
aatgctttat ttattttatt gggctacatt gtaagatcca tctacacagt cgttgtccga 1730
cttcacttga tactatatga tatgaacctt ttttgggtgg ggggtgcngg gcaattccac 1790
tctgtctccc aggetggagt gcaatgggtc aatcttggct cactatagcc ttgacctctg 1850
aggetcaagc gattctctca cctcagccat ccaaatagct gggaccacag gtgtgcacca 1910
ccacgccccg ctaatttttt gtattttgtc taaatataag ggctctctat gttgtctcagg 1970
gtggtctcga attcctggac tcaagcagtc tgcccacyc agactcccaa agcgggtggaa 2030
ttagargcgt gagcccccat gcttggcctt acctttctac yttttataat tctgtatggt 2090
attattttat gaacatgaag aaacttttagt aaatgtactt gtttacatag ttatgtgaat 2150
agattagata aacataaaaag gaggagacat acaatggggg aagaagaaga agtcccctgt 2210
aagaagttna cgntctgggt tccagccttc cctcagatgt actttggctt caatgattgg 2270
caacttctac agggggccagt cttttgaact ggacaacctt acaagtatat gagtattatt 2330
tataggtagt tgtttacata tgagtcggga ccaaagagaa ctggatccac gtgaagtcct 2390
gtgtgtggct ggctccctacc tgggcagctc catttgcacc catagcccc atctatggac 2450
aggetgggac agaggcagat ggggttagatc acacataaca atagggtcta tgtcatatcc 2510
caagtgaact tgagccctgt ttgggctcag gagatagaag acaaaatctg tctcccacgt 2570
ctgccatggc atcaaggggg aagagtagat ggtgcttgag aatgggtgta aatggttgct 2630
atctcaggag tagatggccc ggctcacttc tggttatctg tcaccctgag cccatgagct 2690
gccttttagg gtacagattg cctacttgag gaccttggcc gctctgtaag catctgactc 2750
atctcagaaa tgtcaattct taaacactgt ggcaacagga cctagaatgg ctgacgcatt 2810
aagggtttct tcttgtgtcc tgttctatta ttgttttaag acctcagtaa ccatttcagc 2870
ctctttccag caaacccttc tccatagtat ttcagtcatg gaaggatcat ttatgcagg 2930
agtcattcca ggagtttttg gtcttttctg tctcaaggca ttgtgtgttt tgttccggga 2990
ctggtttggg tgggacaaag ttagaattgc ctgaagatca cacattcaga ctgttgtgtc 3050
tgtggagttt taggagtggg ggggtgacct tctggtcttt gcacttccat cctctcccac 3110
ttccatctgg catcccacgc gttgtccctt gcacttctgg aaggcacagg gtgctgctgc 3170
ctcctgggtc ttgccttttg tgggccttct gtgcaggacg ctcagcctca gggctcagaa 3230
ggtgccagtc cgggtcccagg tcccttgtcc cttccacaga ggccttccta gaagatgcat 3290
ctagagtgtc agccttatca gtgtttaaga tttttctttt atttttaatt tttttgagac 3350
agaatctcac tctctcgccc aggetggagt gcaacggtae gatcttggct cagtgcgaacc 3410
tccgcctcct gggttcaagc gattctctgt cctcagcctc cggagtagct gggattgcag 3470
gcacccgcca ccacgcctgg ttaatttttg tatttttagt agagacgggg tttcaccatg 3530
ttggtcaggc tgggtctcga ctcctgacct cagggtgatc accttggcct ccgaaagtgc 3590
tgggattaca ggcgtgagcc accagccagg ccaagctatt cttttaaagt aagcttctc 3650
acgacatgaa ataattgggg gttttgttgt ttagttacat taggctttgc tatatcccca 3710
ggccaaatag catgtgacac aggacagcca tagtatagtg tgtcactcgt ggttgggtgc 3770
ctttcatgct tctgccctgt caaagggtccc tatttgaaat gtgttataat acaaacagg 3830
aagcacattg tgtacaaaaa acttatgtat ttatgaatcc atgacaaaat taaatatgaa 3890
accttatata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3950
ggsgggcgcg ccgc 3964

```

<210> 6

<211> 411

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
  1           5           10           15
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
      20           25           30
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
      35           40           45

```

```

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
  50                      55                      60
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
  65                      70                      75                      80
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
                      85                      90                      95
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
          100                      105                      110
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
          115                      120                      125
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
          130                      135                      140
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
          145                      150                      155                      160
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
          165                      170                      175
Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
          180                      185                      190
Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
          195                      200                      205
Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
          210                      215                      220
Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
          225                      230                      235                      240
Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
          245                      250                      255
Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
          260                      265                      270
Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
          275                      280                      285
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
          290                      295                      300
Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
          305                      310                      315                      320
Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
          325                      330                      335
Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
          340                      345                      350
Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
          355                      360                      365
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
          370                      375                      380
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
          385                      390                      395                      400
Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
          405                      410

```

```

<210> 7
<211> 2135
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (182) ... (850)

```

```

<400> 7

```

ccacgcgtcc gcgcggggcgc tgcgctgagg ggacggcgagg aggcgcgggcc tggcctcgca 60
 ctcaaagccg ccgcagcgcg ccccgggctc ggccgaccgc gcggggatct aggggtgggc 120
 gacttcgcgg gaccgtggcg catgtttcct gggagttact gatcatcttc tttgaagaaa 180
 c atg aag tta cac tat gtt gct gtg ctt act cta gcc atc ctg atg ttc 229
 Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile Leu Met Phe
 1 5 10 15

 ctg aca tgg ctt cca gaa tca ctg agc tgt aac aaa gca ctc tgt gct 277
 Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala Leu Cys Ala
 20 25 30

 agt gat gtg agc aaa tgc ctc att cag gag ctc tgc cag tgc cgg ccg 325
 Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro
 35 40 45

 gga gaa ggc aat tgc tcc tgc tgt aag gag tgc atg ctg tgt ctt ggg 373
 Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu Cys Leu Gly
 50 55 60

 gcc ctt tgg gac gag tgc tgt gac tgt gtt ggt atg tgt aat cct cga 421
 Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg
 65 70 75 80

 aat tat agt gac aca cct cca act tca aag agc aca gtg gag gag ctg 469
 Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu
 85 90 95

 cat gaa ccg atc cct tct ctc ttc cgg gca ctc aca gaa gga gat act 517
 His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr
 100 105 110

 cag ttg aat tgg aac atc gtt tct ttc cct gtt gca gaa gaa ctt tca 565
 Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser
 115 120 125

 cat cat gag aat ctg gtt tca ttt tta gaa act gtg aac cag cca cac 613
 His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Pro His
 130 135 140

 cac cag aat gtg tct gtc ccc agc aat aat gtt cac gcg cct tat tcc 661
 His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Tyr Ser
 145 150 155 160

 agt gac aaa gaa cac atg tgt act gtg gtt tat ttt gat gac tgc atg 709
 Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met
 165 170 175

 tcc ata cat cag tgt aaa ata tcc tgt gag tcc atg gga gca tcc aaa 757
 Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys
 180 185 190

 tat cgc tgg ttt cat aat gcc tgc tgc gag tgc att ggt cca gaa tgt 805
 Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys
 195 200 205

 att gac tat ggt agt aaa act gtc aaa tgt atg aac tgc atg ttt 850
 Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe

220

```
<210> 8
<211> 223
<212> PRT
<213> Homo sapiens
```

Met	Lys	Leu	His	Tyr	Val	Ala	Val	Leu	Thr	Leu	Ala	Ile	Leu	Met	Phe
1				5					10					15	
Leu	Thr	Trp	Leu	Pro	Glu	Ser	Leu	Ser	Cys	Asn	Lys	Ala	Leu	Cys	Ala
			20					25					30		
Ser	Asp	Val	Ser	Lys	Cys	Leu	Ile	Gln	Glu	Leu	Cys	Gln	Cys	Arg	Pro
		35					40					45			
Gly	Glu	Gly	Asn	Cys	Ser	Cys	Cys	Lys	Glu	Cys	Met	Leu	Cys	Leu	Gly
		50				55					60				
Ala	Leu	Trp	Asp	Glu	Cys	Cys	Asp	Cys	Val	Gly	Met	Cys	Asn	Pro	Arg
65					70					75					80
Asn	Tyr	Ser	Asp	Thr	Pro	Pro	Thr	Ser	Lys	Ser	Thr	Val	Glu	Glu	Leu
				85					90					95	
His	Glu	Pro	Ile	Pro	Ser	Leu	Phe	Arg	Ala	Leu	Thr	Glu	Gly	Asp	Thr
			100					105					110		
Gln	Leu	Asn	Trp	Asn	Ile	Val	Ser	Phe	Pro	Val	Ala	Glu	Glu	Leu	Ser
		115					120					125			
His	His	Glu	Asn	Leu	Val	Ser	Phe	Leu	Glu	Thr	Val	Asn	Gln	Pro	His
		130				135					140				
His	Gln	Asn	Val	Ser	Val	Pro	Ser	Asn	Asn	Val	His	Ala	Pro	Tyr	Ser
145					150					155				160	
Ser	Asp	Lys	Glu	His	Met	Cys	Thr	Val	Val	Tyr	Phe	Asp	Asp	Cys	Met
				165					170					175	
Ser	Ile	His	Gln	Cys	Lys	Ile	Ser	Cys	Glu	Ser	Met	Gly	Ala	Ser	Lys
			180					185					190		
Tyr	Arg	Trp	Phe	His	Asn	Ala	Cys	Cys	Glu	Cys	Ile	Gly	Pro	Glu	Cys
		195					200					205			

Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe
 210 215 220

<210> 9

<211> 3037

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(2601)

<400> 9

atg ccg agc ctc ccg gcc ccg ccg gcc ccg ctg ctg ctc ctc ggg ctg	48
Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Leu Leu Leu Leu Gly Leu	
1 5 10 15	
ctg ctg ctc ggc tcc cgg ccg gcc cgc ggc gcc ggc cca gag ccc ccc	96
Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu Pro Pro	
20 25 30	
gtg ctg ccc atc cgt tct gag aag gag ccg ctg ccc gtt cgg gga gcg	144
Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val Arg Gly Ala	
35 40 45	
gca ggc tgc acc ttc ggc ggg aag gtc tat gcc ttg gac gag acg tgg	192
Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu Asp Glu Thr Trp	
50 55 60	
cac ccg gac cta ggg gag cca ttc ggg gtg atg cgc tgc gtg ctg tgc	240
His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys	
65 70 75 80	
gcc tgc gag gcg cct cag tgg ggt cgc cgt acc agg ggc cct ggc agg	288
Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg Thr Arg Gly Pro Gly Arg	
85 90 95	
gtc agc tgc aag aac atc aaa cca gag tgc cca acc ccg gcc tgt ggg	336
Val Ser Cys Lys Asn Ile Lys Pro Glu Cys Pro Thr Pro Ala Cys Gly	
100 105 110	
cag ccg cgc cag ctg ccg gga cac tgc tgc cag acc tgc ccc cag gag	384
Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu	
115 120 125	
cgc agc agt tcg gag ccg cag ccg agc ggc ctg tcc ttc gag tat ccg	432
Arg Ser Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu Tyr Pro	
130 135 140	
cgg gac ccg gag cat cgc agt tat agc gac cgc ggg gag cca ggc gct	480
Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala	
145 150 155 160	
gag gag ccg gcc cgt ggt gac ggc cac acg gac ttc gtg gcg ctg ctg	528
Glu Glu Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu	
165 170 175	

aca ggg ccg agg tcg cag gcg gtg gca cga gcc cga gtc tcg ctg ctg	576
Thr Gly Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu	
180 185 190	
cgc tct agc ctc cgc ttc tct atc tcc tac agg cgg ctg gac cgc cct	624
Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro	
195 200 205	
acc agg atc cgc ttc tca gac tcc aat ggc agt gtc ctg ttt gag cac	672
Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His	
210 215 220	
cct gca gcc ccc acc caa gat ggc ctg gtc tgt ggg gtg tgg cgg gca	720
Pro Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala	
225 230 235 240	
gtg cct cgg ttg tct ctg cgg ctc ctt agg gca gaa cag ctg cat gtg	768
Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His Val	
245 250 255	
gca ctt gtg aca ctc act cac cct tca ggg gag gtc tgg ggg cct ctc	816
Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu	
260 265 270	
atc cgg cac cgg gcc ctg gct gca gag acc ttc agt gcc atc ctg act	864
Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr	
275 280 285	
cta gaa ggc ccc cca cag cag ggc gta ggg ggc atc acc ctg ctc act	912
Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile Thr Leu Leu Thr	
290 295 300	
ctc agt gac aca gag gac tcc ttg cat ttt ttg ctg ctc ttc cga ggg	960
Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe Arg Gly	
305 310 315 320	
ctg ctg gaa ccc agg agt ggg gga cta acc cag gtt ccc ttg agg ctc	1008
Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr Gln Val Pro Leu Arg Leu	
325 330 335	
cag att cta cac cag ggg cag cta ctg cga gaa ctt cag gcc aat gtc	1056
Gln Ile Leu His Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala Asn Val	
340 345 350	
tca gcc cag gaa cca ggc ttt gct gag gtg ctg ccc aac ctg aca gtc	1104
Ser Ala Gln Glu Pro Gly Phe Ala Glu Val Leu Pro Asn Leu Thr Val	
355 360 365	
cag gag atg gac tgg ctg gtg ctg ggg gag ctg cag atg gcc ctg gag	1152
Gln Glu Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala Leu Glu	
370 375 380	
tgg gca ggc agg cca ggg ctg cgc atc agt gga cac att gct gcc agg	1200
Trp Ala Gly Arg Pro Gly Leu Arg Ile Ser Gly His Ile Ala Ala Arg	
385 390 395 400	
aag agc tgc gac gtc ctg caa agt gtc ctt tgt ggg gct gat gcc ctg	1248

Lys Ser Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu	
405 410 415	
atc cca gtc cag acg ggt gct gcc ggc tca gcc agc ctc acg ctg cta	1296
Ile Pro Val Gln Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu	
420 425 430	
gga aat ggc tcc ctg atc tat cag gtg caa gtg gta ggg aca agc agt	1344
Gly Asn Gly Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser	
435 440 445	
gag gtg gtg gcc atg aca ctg gag acc aag cct cag cgg agg gat cag	1392
Glu Val Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln	
450 455 460	
cgc act gtc ctg tgc cac atg gct gga ctc cag cca gga gga cac acg	1440
Arg Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr	
465 470 475 480	
gcc gtg ggt atc tgc cct ggg ctg ggt gcc cga ggg gct cat atg ctg	1488
Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met Leu	
485 490 495	
ctg cag aat gag ctc ttc ctg aac gtg ggc acc aag gac ttc cca gac	1536
Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe Pro Asp	
500 505 510	
gga gag ctt cgg ggg cac gtg gct gcc ctg ccc tac tgt ggg cat agc	1584
Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys Gly His Ser	
515 520 525	
gcc cgc cat gac acg ctg tcc gtg ccc cta gca gga gcc ctg gtg cta	1632
Ala Arg His Asp Thr Leu Ser Val Pro Leu Ala Gly Ala Leu Val Leu	
530 535 540	
ccc cct gtg aag agc caa gca gca ggg cac gcc tgg ctt tcc ttg gat	1680
Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala Trp Leu Ser Leu Asp	
545 550 555 560	
acc cac tgt cac ctg cac tat gaa gtg ctg ctg gct ggg ctt ggt ggc	1728
Thr His Cys His Leu His Tyr Glu Val Leu Leu Ala Gly Leu Gly Gly	
565 570 575	
tca gaa caa ggc act gtc act gcc cac ctc ctt ggg cct cct gga acg	1776
Ser Glu Gln Gly Thr Val Thr Ala His Leu Leu Gly Pro Pro Gly Thr	
580 585 590	
cca ggg cct cgg cgg ctg ctg aag gga ttc tat ggc tca gag gcc cag	1824
Pro Gly Pro Arg Arg Leu Leu Lys Gly Phe Tyr Gly Ser Glu Ala Gln	
595 600 605	
ggt gtg gtg aag gac ctg gag ccg gaa ctg ctg cgg cac ctg gca aaa	1872
Gly Val Val Lys Asp Leu Glu Pro Glu Leu Leu Arg His Leu Ala Lys	
610 615 620	
ggc atg gcc tcc ctg atg atc acc acc aag ggt agc ccc aga ggg gag	1920
Gly Met Ala Ser Leu Met Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu	

625	630	635	640	
ctc cga ggg cag aga cga acg gtg atc tgt gac ccg gtg gtg tgc cca				1968
Leu Arg Gly Gln Arg Arg Thr Val Ile Cys Asp Pro Val Val Cys Pro				
	645	650	655	
ccg ccc agc tgc cca cac ccg gtg cag gct ccc gac cag tgc tgc cct				2016
Pro Pro Ser Cys Pro His Pro Val Gln Ala Pro Asp Gln Cys Cys Pro				
	660	665	670	
gtt tgc cct gag aaa caa gat gtc aga gac ttg cca ggg ctg cca agg				2064
Val Cys Pro Glu Lys Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg				
	675	680	685	
agc cgg gac cca gga gag ggc tgc tat ttt gat ggt gac cgg agc tgg				2112
Ser Arg Asp Pro Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp				
	690	695	700	
cgg gca gcg ggt acg cgg tgg cac ccc gtt gtg ccc ccc ttt ggc tta				2160
Arg Ala Ala Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu				
	705	710	715	720
att aag tgt gct gtc tgc acc tgc aag ggg ggc act gga gag gtg cac				2208
Ile Lys Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His				
	725	730	735	
tgt gag aag gtg cag tgt ccc cgg ctg gcc tgt gcc cag cct gtg cgt				2256
Cys Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg				
	740	745	750	
gtc aac ccc acc gac tgc tgc aaa cag tgt cca gtg ggg tcg ggg gcc				2304
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly Ala				
	755	760	765	
cac ccc cag ctg ggg gac ccc atg cag gct gat ggg ccc cgg ggc tgc				2352
His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg Gly Cys				
	770	775	780	
cgt ttt gct ggg cag tgg ttc cca gag agt cag agc tgg cac ccc tca				2400
Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp His Pro Ser				
	785	790	795	800
gtg ccc cct ttt gga gag atg agc tgt atc acc tgc aga tgt ggg gca				2448
Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys Arg Cys Gly Ala				
	805	810	815	
ggg gtg cct cac tgt gag cgg gat gac tgt tca ctg cca ctg tcc tgt				2496
Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser Leu Pro Leu Ser Cys				
	820	825	830	
ggc tcg ggg aag gag agt cga tgc tgt tcc cgc tgc acg gcc cac cgg				2544
Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser Arg Cys Thr Ala His Arg				
	835	840	845	
cgg cca gcc cca gag acc aga act gat cca gag ctg gag aaa gaa gcc				2592
Arg Pro Ala Pro Glu Thr Arg Thr Asp Pro Glu Leu Glu Lys Glu Ala				
	850	855	860	

gaa ggc tct tagggagcag ccagagggcc aagtgaccaa gaggatgggg
 Glu Gly Ser
 865

2641

cctgagctgg ggaaggggtg gcatcgagga ccttcttgca ttctcctgtg ggaagcccag 2701
 tgccttttgc cctctgtcct gcctctactc ccacccccac tacctttggg aaccacagct 2761
 ccacaagggg gagaggcagc tgggccagac cgaggtcaca gccactccaa gtccctgcct 2821
 gccaccctcg gcctctgtcc ttggaagccc cacccttttc ctccctgtaca taatgtcact 2881
 ggcttggttg gatttttaaat ttatcttcac tcagcaccaa gggccccga cactccactc 2941
 ctgctgcccc tgagctgagc agagtcatta ttggagagtt ttgtatttat taaaacattt 3001
 ctttttcagt caaaaaaaaa aaaaaagggc ggccgc 3037

<210> 10

<211> 867

<212> PRT

<213> Homo sapiens

<400> 10

Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Leu Leu Leu Leu Gly Leu
 1 5 10 15
 Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu Pro Pro
 20 25 30
 Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val Arg Gly Ala
 35 40 45
 Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu Asp Glu Thr Trp
 50 55 60
 His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys
 65 70 75 80
 Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg Thr Arg Gly Pro Gly Arg
 85 90 95
 Val Ser Cys Lys Asn Ile Lys Pro Glu Cys Pro Thr Pro Ala Cys Gly
 100 105 110
 Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu
 115 120 125
 Arg Ser Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu Tyr Pro
 130 135 140
 Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala
 145 150 155 160
 Glu Glu Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu
 165 170 175
 Thr Gly Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu
 180 185 190
 Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro
 195 200 205
 Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His
 210 215 220
 Pro Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
 225 230 235 240
 Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His Val
 245 250 255
 Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu
 260 265 270
 Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr
 275 280 285
 Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile Thr Leu Leu Thr
 290 295 300

Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe Arg Gly
 305 310 315 320
 Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr Gln Val Pro Leu Arg Leu
 325 330 335
 Gln Ile Leu His Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala Asn Val
 340 345 350
 Ser Ala Gln Glu Pro Gly Phe Ala Glu Val Leu Pro Asn Leu Thr Val
 355 360 365
 Gln Glu Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala Leu Glu
 370 375 380
 Trp Ala Gly Arg Pro Gly Leu Arg Ile Ser Gly His Ile Ala Ala Arg
 385 390 395 400
 Lys Ser Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu
 405 410 415
 Ile Pro Val Gln Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu
 420 425 430
 Gly Asn Gly Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser
 435 440 445
 Glu Val Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln
 450 455 460
 Arg Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr
 465 470 475 480
 Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met Leu
 485 490 495
 Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe Pro Asp
 500 505 510
 Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys Gly His Ser
 515 520 525
 Ala Arg His Asp Thr Leu Ser Val Pro Leu Ala Gly Ala Leu Val Leu
 530 535 540
 Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala Trp Leu Ser Leu Asp
 545 550 555 560
 Thr His Cys His Leu His Tyr Glu Val Leu Leu Ala Gly Leu Gly Gly
 565 570 575
 Ser Glu Gln Gly Thr Val Thr Ala His Leu Leu Gly Pro Pro Gly Thr
 580 585 590
 Pro Gly Pro Arg Arg Leu Leu Lys Gly Phe Tyr Gly Ser Glu Ala Gln
 595 600 605
 Gly Val Val Lys Asp Leu Glu Pro Glu Leu Leu Arg His Leu Ala Lys
 610 615 620
 Gly Met Ala Ser Leu Met Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu
 625 630 635 640
 Leu Arg Gly Gln Arg Arg Thr Val Ile Cys Asp Pro Val Val Cys Pro
 645 650 655
 Pro Pro Ser Cys Pro His Pro Val Gln Ala Pro Asp Gln Cys Cys Pro
 660 665 670
 Val Cys Pro Glu Lys Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg
 675 680 685
 Ser Arg Asp Pro Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp
 690 695 700
 Arg Ala Ala Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu
 705 710 715 720
 Ile Lys Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His
 725 730 735
 Cys Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg
 740 745 750
 Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly Ala

755 760 765
 His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg Gly Cys
 770 775 780
 Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp His Pro Ser
 785 790 795 800
 Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys Arg Cys Gly Ala
 805 810 815
 Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser Leu Pro Leu Ser Cys
 820 825 830
 Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser Arg Cys Thr Ala His Arg
 835 840 845
 Arg Pro Ala Pro Glu Thr Arg Thr Asp Pro Glu Leu Glu Lys Glu Ala
 850 855 860
 Glu Gly Ser
 865

<210> 11

<211> 940

<212> PRT

<213> *Xenopus laevis*

<400> 11

Gln Cys Pro Pro Ile Leu Leu Val Trp Thr Leu Trp Ile Met Ala Val
 1 5 10 15
 Asp Cys Ser Arg Pro Lys Val Phe Leu Pro Ile Gln Pro Glu Gln Glu
 20 25 30
 Pro Leu Gln Ser Lys Thr Pro Ala Gly Cys Thr Phe Gly Gly Lys Phe
 35 40 45
 Tyr Ser Leu Glu Asp Ser Trp His Pro Asp Leu Gly Glu Pro Phe Gly
 50 55 60
 Val Met His Cys Val Leu Cys Tyr Cys Glu Pro Gln Arg Ser Arg Arg
 65 70 75 80
 Gly Lys Pro Ser Gly Lys Val Ser Cys Lys Asn Ile Lys His Asp Cys
 85 90 95
 Pro Ser Pro Ser Cys Ala Asn Pro Ile Leu Leu Pro Leu His Cys Cys
 100 105 110
 Lys Thr Cys Pro Lys Ala Pro Pro Pro Ile Lys Lys Ser Asp Phe
 115 120 125
 Val Phe Asp Gly Phe Glu Tyr Phe Gln Glu Lys Asp Asp Asp Leu Tyr
 130 135 140
 Asn Asp Arg Ser Tyr Leu Ser Ser Asp Asp Val Ala Val Glu Glu Ser
 145 150 155 160
 Arg Ser Glu Tyr Val Ala Leu Leu Thr Ala Pro Ser His Val Trp Pro
 165 170 175
 Pro Val Thr Ser Gly Val Ala Lys Ala Arg Phe Asn Leu Gln Arg Ser
 180 185 190
 Asn Leu Leu Phe Ser Ile Thr Tyr Lys Trp Ile Asp Arg Leu Ser Arg
 195 200 205
 Ile Arg Phe Ser Asp Leu Asp Gly Ser Val Leu Phe Glu His Pro Val
 210 215 220
 His Arg Met Gly Ser Pro Arg Asp Asp Thr Ile Cys Gly Ile Trp Arg
 225 230 235 240
 Ser Leu Asn Arg Ser Thr Leu Arg Leu Leu Arg Met Gly His Ile Leu
 245 250 255
 Val Ser Leu Val Thr Thr Thr Leu Ser Glu Pro Glu Ile Ser Gly Lys
 260 265 270
 Ile Val Lys His Lys Ala Leu Phe Ser Glu Ser Phe Ser Ala Leu Leu

[illegible]

Gln Pro Val His Leu Pro Asp Gln Cys Cys Pro Val Cys Glu Glu Lys
 740 745 750
 Lys Glu Met Arg Glu Val Lys Lys Pro Glu Arg Ala Arg Thr Ser Glu
 755 760 765
 Gly Cys Phe Phe Asp Gly Asp Arg Ser Trp Lys Ala Ala Gly Thr Arg
 770 775 780
 Trp His Pro Phe Val Pro Pro Phe Gly Leu Ile Lys Cys Ala Ile Cys
 785 790 795 800
 Thr Cys Lys Gly Ser Thr Gly Glu Val His Cys Glu Lys Val Thr Cys
 805 810 815
 Pro Lys Leu Ser Cys Thr Asn Pro Ile Arg Ala Asn Pro Ser Asp Cys
 820 825 830
 Cys Lys Gln Cys Pro Val Glu Glu Arg Ser Pro Met Glu Leu Ala Asp
 835 840 845
 Ser Met Gln Ser Asp Gly Ala Gly Ser Cys Arg Phe Gly Arg His Trp
 850 855 860
 Tyr Pro Asn His Glu Arg Trp His Pro Thr Val Pro Pro Phe Gly Glu
 865 870 875 880
 Met Lys Cys Val Thr Cys Thr Cys Ala Glu Gly Ile Thr Gln Cys Arg
 885 890 895
 Arg Gln Glu Cys Thr Gly Thr Thr Cys Gly Thr Gly Ser Lys Arg Asp
 900 905 910
 Arg Cys Cys Thr Lys Cys Lys Asp Ala Asn Gln Asp Glu Asp Glu Lys
 915 920 925
 Val Lys Ser Asp Glu Thr Arg Thr Pro Trp Ser Phe
 930 935 940

<210> 12
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 12
 cgggatccgg ccctacggc gccaacatg

29

<210> 13
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 13
 cggaattctc attggctcag cttattgaga atcat

35

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 14
 catggcggtgta gggaacgctc t 21

<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 15
 gttctgtccc cgttgttcca t 21

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 16
 ggcttcccca ctgtgctttg t 21

<210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 17
 ggaggtcacc gtctcctcca c 21

<210> 18
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 18
 atggaacaac ggggacag 18

<210> 19
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 19
 ttcttcgcac tgacacac 18

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 20
 atgtcattgt tttcacagca 20

<210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 21
 gctcaagcga ttctctca 18

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 22
 tgcagtcagt aggcgagcca t 21

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 23
 gtaatcacgg cagcagacgc t 21

<210> 24
 <211> 2601
 <212> DNA
 <213> Homo sapiens

<400> 24
 atgccgagcc tcccggcccc gcgggccccg ctgctgctcc tggggctgct gctgctcggc 60
 tcccggccgg cccgcggcgc cggcccagag cccccctgc tgcccatccg ttctgagaag 120
 gagccgctgc ccgttcgggg agcggcaggc tgcaccttcg gcgggaaggt ctatgccttg 180
 gacgagacgt ggcacccgga cctaggggag ccattcgggg tgatgcgctg cgtgctgtgc 240
 gcctgcgagg cgcctcagtg gggtcgccgt accagggggc ctggcagggt cagctgcaag 300
 aacatcaaac cagagtgcc aaccccggcc tgtgggcagc cgcgccagct gccgggacac 360

tgctgccaga	cctgccccca	ggagcgcagc	agttcggagc	ggcagccgag	cggcctgtcc	420
tteagagtac	cgcggggaccc	ggagcatcgc	agttatagcg	accgcgggga	gccaggcgct	480
gaggagcggg	cccgtggtga	cggccacacg	gacttcgtgg	cgctgctgac	agggccgagg	540
tgcaggcgg	tggcacgagc	ccgagtctcg	ctgctgcgct	ctagcctccg	cttctctatc	600
tcctacaggc	ggctggaccg	ccctaccagg	atccgcttct	cagactccaa	tggcagtgtc	660
ctggtttgagc	accctgcagc	ccccacccaa	gatggcctgg	tctgtggggg	gtggcgggca	720
gtgcctcggt	tgtctctgcg	gctccttagg	gcagaacagc	tgcattgtggc	acttgtgaca	780
ctcactcacc	cttcaggggga	ggtctggggg	cctctcatcc	ggcacccggc	cctggctgca	840
gagaccttca	gtgccatcct	gactctagaa	ggccccccac	agcaggggcgt	agggggcatc	900
accctgetca	ctctcagtga	cacagaggac	tccttgctatt	ttttgctgct	cttccgaggg	960
ctgctggaac	ccaggagtgg	gggactaacc	caggttccct	tgaggctcca	gattctacac	1020
caggggcagc	tactgcgaga	acttcaggcc	aatgtctcag	cccaggaacc	aggctttgct	1080
gagggtgctgc	ccaacctgac	agtccaggag	atggactggc	tgggtgctggg	ggagctgcag	1140
atggccctgg	agtgggcagg	caggccaggg	ctgcgcacat	gtggacacat	tgctgccagg	1200
aagagctgcg	acgtcctgca	aagtgtcctt	tgtggggctg	atgccctgat	cccagtccag	1260
acgggtgctg	ccggctcagc	cagcctcacg	ctgctaggaa	atggctccct	gatctatcag	1320
gtgcaagtgg	tagggacaag	cagtggagtg	gtggccatga	cactggagac	caagcctcag	1380
cggaggggac	agcgcactgt	cctgtgccac	atggctggac	tccagccagg	aggacacacg	1440
gccgtgggta	tctgccctgg	gctgggtgcc	cgaggggctc	atatgctgct	gcagaatgag	1500
ctcttcctga	acgtgggcac	caaggacttc	ccagacggag	agcttcgggg	gcacgtggct	1560
gccctgccct	actgtgggca	tagcgcccg	catgacacgc	tgtccgtgcc	cctagcagga	1620
gccctgggtg	tacccccctgt	gaagagccaa	gcagcagggc	acgcctggct	ttccttggat	1680
accactgtc	acctgcacta	tgaagtgtcg	ctggctgggc	ttgggtggctc	agaacaaggc	1740
actgtcactg	cccacctcct	tgggcctcct	ggaacgccag	ggcctcggcg	gctgctgaag	1800
ggattctatg	gctcagaggc	ccagggtgtg	gtgaaggacc	tggagccgga	actgctgcgg	1860
cacctggcaa	aaggcatggc	ctccctgatg	atcaccacca	agggtagccc	cagaggggag	1920
ctccgagggc	agagacgaac	ggtgatctgt	gaccgggtgg	tgtgcccacc	gccagctgc	1980
ccacacccgg	tgcaggctcc	cgaccagtgc	tgcctgtttt	gccctgagaa	acaagatgtc	2040
agagacttgc	cagggctgcc	aaggagccgg	gaccagggag	agggctgcta	ttttgatggt	2100
gaccggagct	ggcgggcagc	gggtacgcgg	tggcaccccg	ttgtgcccc	ctttggctta	2160
attaagtgtg	ctgtctgcac	ctgcaagggg	ggcactggag	aggtgactg	tgagaagggtg	2220
cagtgtcccc	ggctggcctg	tgcccagcct	gtgcgtgtca	acccaccga	ctgctgcaaa	2280
cagtgtccag	tggggtcggg	ggcccacccc	cagctggggg	accccatgca	ggctgatggg	2340
ccccggggct	gccgttttgc	tgggcagtgg	ttcccagaga	gtcagagctg	gcacccctca	2400
gtgccccctt	ttggagagat	gagctgtatc	acctgcagat	gtggggcagg	ggtgcctcac	2460
tgtgagcggg	atgactgttc	actgccactg	tcctgtggct	cggggaagga	gagtcgatgc	2520
tgttcccgc	gcacggccca	ccggcgccca	gccccagaga	ccagaactga	tccagagctg	2580
gagaaagaag	ccgaaggctc	t				2601